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PCT09

RAW SEQUENCE LISTING DATE: 12/21/2001
PATENT APPLICATION: US/09/744,226A TIME: 13:10:09

Input Set : A:\2534seq.txt
Output Set: N:\CRF3\12212001\I744226A.raw

ENTERED

<110> APPLICANT: OHARA, Osamu
NAGASE, Takahiro
NOMURA, Nobuo
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KITAHARA, Osamu
MOGI, Shinichi
<120> TITLE OF INVENTION: Novel G Protein Coupled Receptor Protein and Its DNA
<130> FILE REFERENCE: 2534 US0P
<140> CURRENT APPLICATION NUMBER: US 09/744,226A
<141> CURRENT FILING DATE: 2001-01-22
<150> PRIOR APPLICATION NUMBER: PCT/JP99/03909
<151> PRIOR FILING DATE: 1998-07-22
<150> PRIOR APPLICATION NUMBER: JP 10-207579
<151> PRIOR FILING DATE: 1998-07-23
<150> PRIOR APPLICATION NUMBER: JP 10-225060
<151> PRIOR FILING DATE: 1998-08-07
<150> PRIOR APPLICATION NUMBER: JP 10-284328
<151> PRIOR FILING DATE: 1998-10-06
<160> NUMBER OF SEQ ID NOS: 9
<170> SOFTWARE: PatentIn version 3.0
<210> SEQ ID NO: 1
<211> LENGTH: 872
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1

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            20                  25                  30
Asn Leu Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu Asn Lys
        35                  40                  45
Ala Met Val Glu Thr Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn
    50                  55                  60
Ala Trp Arg Asp Leu Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met
65                  70                  75                  80
Leu Leu His Thr Val Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu
                85                  90                  95
Leu Lys Thr Asp Ile Val Arg Glu Asn Thr Asp Asn Ile Lys Leu Glu
            100                 105                 110
Val Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro
        115                 120                 125
Glu Asn Met Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu
    130                 135                 140
Lys Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr
145                 150                 155                 160
Asn Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu
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72                  165                 170                 175
74 Gly Thr Glu Ala Leu Ser Thr Asn His Ser Val Ile Val Asn Ser Pro
75              180                 185                 190
77 Val Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu
78          195                 200                 205
80 Ala Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu
81      210                 215                 220
83 Asn Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met
84 225                 230                 235                 240
86 Thr Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys
87                  245                 250                 255
89 Thr His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu
90              260                 265                 270
92 Met Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu
93          275                 280                 285
95 Leu Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu
96      290                 295                 300
98 Leu Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp
99 305                 310                 315                 320
101 Arg Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu
102                 325                 330                 335
104 Leu Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys
105             340                 345                 350
107 Ala Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr
108         355                 360                 365
110 Trp Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val
111     370                 375                 380
113 Phe Glu Ser Glu His Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr
114 385                 390                 395                 400
116 Gly Met Pro Ala Leu Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg
117                 405                 410                 415
119 Ser Tyr Gly Thr Asp Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe
120             420                 425                 430
122 Ile Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val
123         435                 440                 445
125 Ile Phe Leu Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile
126     450                 455                 460
128 Leu Lys Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile
129 465                 470                 475                 480
131 Gly Ala Ile Ala Leu Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly
132                 485                 490                 495
134 Leu Met Tyr Ile Asn Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr
135             500                 505                 510
137 Ile Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His Cys Val
138         515                 520                 525
140 Leu Gln Lys Lys Val Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His
141     530                 535                 540
143 Cys Cys Ser Gly Lys Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr
144 545                 550                 555                 560
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147                 565                 570                 575
149 Ile Arg Arg Met Trp Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser
150             580                 585                 590
152 Phe Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Gly
153         595                 600                 605
155 Leu Leu Asn Asn Ala Arg Asp Thr Ser Val Met Asp Thr Leu Pro Leu
156     610                 615                 620
158 Asn Gly Asn His Gly Asn Ser Tyr Ser Ile Ala Ser Gly Glu Tyr Leu
159 625                 630                 635                 640
161 Ser Asn Cys Val Gln Ile Ile Asp Arg Gly Tyr Asn His Asn Glu Thr
162                 645                 650                 655
164 Ala Leu Glu Lys Lys Ile Leu Lys Glu Leu Thr Ser Asn Tyr Ile Pro
165             660                 665                 670
167 Ser Tyr Leu Asn Asn His Glu Arg Ser Ser Glu Gln Asn Arg Asn Leu
168         675                 680                 685
170 Met Asn Lys Leu Val Asn Asn Leu Gly Ser Gly Arg Glu Asp Asp Ala
171     690                 695                 700
173 Ile Val Leu Asp Asp Ala Thr Ser Phe Asn His Glu Glu Ser Leu Gly
174 705                 710                 715                 720
176 Leu Glu Leu Ile His Glu Glu Ser Asp Ala Pro Leu Leu Pro Pro Arg
177                 725                 730                 735
179 Val Tyr Ser Thr Glu Asn His Gln Pro His His Tyr Thr Arg Arg Arg
180             740                 745                 750
182 Ile Pro Gln Asp His Ser Glu Ser Phe Phe Pro Leu Leu Thr Asn Glu
183         755                 760                 765
185 His Thr Glu Asp Leu Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser
186     770                 775                 780
188 Met Pro Thr Leu Ala Gly Val Ala Ala Thr Glu Ser Val Thr Thr Ser
189 785                 790                 795                 800
191 Thr Gln Thr Glu Pro Pro Pro Ala Lys Cys Gly Asp Ala Glu Asp Val
192                 805                 810                 815
194 Tyr Tyr Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Gln
195             820                 825                 830
197 Leu His Thr Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile
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204 865                 870
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207 <211> LENGTH: 2616
208 <212> TYPE: DNA
209 <213> ORGANISM: Homo sapiens
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216 agtgctgccc ggagtttgaa caaggcaatg gtcgagacag ttaacaacct ccttcagcca    180
218 caagctttga atgcatggag agacctgact acgagtgatc agctgcgtgc ggccaccatg    240
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222 attgtcaggg agaatacaga caatattaaa ttggaagttg caagactgag cacagaagga    360
224 aacttagaag acctaaaatt tccagaaaac atgggccatg gaagcactat ccagctgtct    420
226 gcaaatacct taaagcaaaa tggccgaaat ggagagatca gagtggcctt tgtcctgtat    480
228 aacaacttgg gtccttattt atccacggag aatgccagta tgaagttggg aacggaagct    540
230 ttgtccacaa atcattctgt tattgtcaat tcccctgtta ttacggcagc aataaacaaa    600
232 gagttcagta acaaggttta tttggctgat cctgtggtat ttactgttaa acatatcaag    660
234 cagtcagagg aaaatttcaa ccctaactgt tcattttgga gctactccaa gcgtacaatg    720
236 acaggttatt ggtcaacaca aggctgtcgg ctcctgacaa caaataagac acatactaca    780
238 tgctcttgta accacctaac aaattttgca gtactgatgg cacatgtgga agttaagcac    840
240 agtgatgcgg tccatgacct ccttctggat gtgatcacgt gggttggaat tttgctgtcc    900
242 cttgtttgtc tcctgatttg catcttcaca ttttgctttt tccgcgggct ccagagtgac    960
244 cgtaacacca tccacaagaa cctctgcatc agtctctttg tagcagagct gctcttcctg   1020
246 attgggatca accgaactga ccaaccaatt gcctgtgctg ttttcgctgc cctgttttct   1080
248 tcttcttggc tgccttcacc tggatgttcc tggaggggt gcagctttat atacatcatg   1140
250 ctggtggagg tttttgagag tgaacattca cgtaggaaat acttttatct ggtcggctat   1200
252 gggatgcctg cactcattgt ggctgtgtca gctgcagtag actacaggag ttatggaaca   1260
254 gataaagtat gttggctccg acttgacacc tacttcattt ggagttttat aggaccagca   1320
256 actttgataa ttatgcttaa tgtaatcttc cttgggattg ctttatataa aatgtttcat   1380
258 catactgcta tactgaaacc tgaatcaggc tgtcttgata acatcaagtc atgggttata   1440
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262 aatgaaagca cagtcatcat ggcctatctc ttcaccattt tcaattctct acagggaatg   1560
264 tttatattta ttttccattg tgtcctacag aagaaggtac gaaaagagta tgggaaatgc   1620
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280 tccagtgaac agaacaggaa tctgatgaac aagctggtga ataaccttgg cagtggaagg   2100
282 gaagatgatg ccattgtcct ggatgatgcc acctcgttta accacgagga gagtttgggc   2160
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290 ctctatacca gcatgccgac actggctggt gtggccgcca cagagagtgt taccaccagc   2400
292 acccagaccg aacccccacc ggccaaatgt ggtgatgccg aagatgttta ctacaaaagc   2460
294 atgccaaacc taggctccag aaaccacgtc catcagctgc atacttacta ccagctaggt   2520
296 cgcggcagca gtgatggatt tatagttcct ccaaacaaag atgggacccc tcccgaggga   2580
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303 <212> TYPE: PRT
304 <213> ORGANISM: Homo sapiens
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312             20                  25                  30
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314 Ala Leu Asp Ser Lys Gly Ile Lys Trp Pro Gln Thr Gln Arg Gly Met
315         35                  40                  45
317 Met Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Thr Ala Ser Tyr
318     50                  55                  60
320 Leu Cys Met Ile Ser Thr Gly Thr Trp Asn Pro Lys Gly Pro Asp Leu
321 65                  70                  75                  80
323 Ser Asn Cys Thr Ser His Trp Val Asn Gln Leu Ala Gln Lys Ile Arg
324                 85                  90                  95
326 Ser Gly Glu Asn Ala Ala Ser Leu Ala Asn Glu Leu Ala Lys His Thr
327             100                 105                 110
329 Lys Gly Pro Val Phe Ala Gly Asp Val Ser Ser Ser Val Arg Leu Met
330         115                 120                 125
332 Glu Gln Leu Val Asp Ile Leu Asp Ala Gln Leu Gln Glu Leu Lys Pro
333     130                 135                 140
335 Ser Glu Lys Asp Ser Ala Gly Arg Ser Tyr Asn Lys Leu Gln Lys Arg
336 145                 150                 155                 160
338 Glu Lys Thr Cys Arg Ala Tyr Leu Lys Ala Ile Val Asp Thr Val Asp
339                 165                 170                 175
341 Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys His Met Asn Ser
342             180                 185                 190
344 Ser Glu Gln Ala His Thr Ala Thr Met Leu Leu Asp Thr Leu Glu Glu
345         195                 200                 205
347 Gly Ala Phe Val Leu Ala Asp Asn Leu Leu Glu Pro Thr Arg Val Ser
348     210                 215                 220
350 Met Pro Thr Glu Asn Ile Val Leu Glu Val Ala Val Leu Ser Thr Glu
351 225                 230                 235                 240
353 Gly Gln Ile Gln Asp Phe Lys Phe Pro Leu Gly Ile Lys Gly Ala Gly
354                 245                 250                 255
356 Ser Ser Ile Gln Leu Ser Ala Asn Thr Val Lys Gln Asn Ser Arg Asn
357             260                 265                 270
359 Gly Leu Ala Lys Leu Val Phe Ile Ile Tyr Arg Ser Leu Gly Gln Phe
360         275                 280                 285
362 Leu Ser Thr Glu Asn Ala Thr Ile Lys Leu Gly Ala Asp Phe Ile Gly
363     290                 295                 300
365 Arg Asn Ser Thr Ile Ala Val Asn Ser His Val Ile Ser Val Ser Ile
366 305                 310                 315                 320
368 Asn Lys Glu Ser Ser Arg Val Tyr Leu Thr Asp Pro Val Leu Phe Thr
369                 325                 330                 335
371 Leu Pro His Ile Asp Pro Asp Asn Tyr Phe Asn Ala Asn Cys Ser Phe
372             340                 345                 350
374 Trp Asn Tyr Ser Glu Arg Thr Met Met Gly Tyr Trp Ser Thr Gln Gly
375         355                 360                 365
377 Cys Lys Leu Val Asp Thr Asn Lys Thr Arg Thr Thr Cys Ala Cys Ser
378     370                 375                 380
380 His Leu Thr Asn Phe Ala Ile Leu Met Ala His Arg Glu Ile Ala Tyr
381 385                 390                 395                 400
383 Lys Asp Gly Val His Glu Leu Leu Leu Thr Val Ile Thr Trp Val Gly
384                 405                 410                 415
386 Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Phe Thr Phe Cys
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